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FIG. 1

BLASTP 2.2.1 [Jul-12-2001]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),

"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

Query= genscan2

(416 letters)

Database: ncbi-nr

897,014 sequences; 280,886,335 total letters

Searching.....done

	Score	E
Sequences producing significant alignments:	(bits)	Value
pir JC1512 biliary glycoprotein H - mouse	81	2e-14
pir JC1506 biliary glycoprotein B - mouse	81	2e-14
pir A39037 carcinoembryonic antigen mmCGM2 precursor - mouse >g...	79	9e-14
ref NP_036056.1 (NM_011926) CEA-related cell adhesion molecule ...	79	9e-14
pir JC1509 biliary glycoprotein E - mouse	73	5e-12
ref NP_001758.1 (NM_001767) CD2 antigen (p50), sheep red blood ...	73	6e-12
ref NP_113943.1 (NM_031755) carcinoembryonic antigen-related ce...	72	8e-12
pir RWHUC2 T-cell surface glycoprotein CD2 precursor - human >g...	72	8e-12
gb AAA51946.1 (M16336) CD2 surface antigen (Homo sapiens)	72	8e-12
ref NP_291021.1 (NM_033543) hypothetical protein R29124_1 [Homo...	72	1e-11
pir JC1507 biliary glycoprotein C - mouse	71	2e-11
emb CAA47697.1 (X67280) biliary glycoprotein [Mus musculus]	71	2e-11
pir S34338 biliary glycoprotein F - mouse >gi 312586 emb CAA476...	71	2e-11
pir JC1511 biliary glycoprotein G - mouse	71	2e-11

FIG. 1(contd.)

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FIG. 2

>pir||JC1512 biliary glycoprotein H - mouse

Length = 341

Score = 80.9 bits (198), Expect = 2e-14

Identities = 54/168 (32%), Positives = 86/168 (51%), Gaps = 9/168 (5%)

Query: 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTVEVEISITD 128

+ PV+ I +V GT + P + R ++ NGSLL+ + + D G Y +E+ TD

Sbjct: 69 KGNPVSTNAEIVHQVTGTNKTTPAHSGRETVYSNGSLLIQRVTVKDTGVYTIEM--TD 126

Query: 129 DTFTG-EKTINLTVDVPISRPOVLVASTTVLELSEAFTLNCSENGTKPSYTWLKDGP 187

+ F E T+ V P+++P + V +TTV EL ++ TL C N + WL + + L

Sbjct: 127 ENFRTEATVQFHVHPVTQPSLQVTNTTVKEL-DSVTLTCL-SNDIGANIQWLFNSQSL 184

Query: 188 LND SRMLLSPDQKVLITRVLMEDDLYSCMVENPISQGRSLPVKITV 235

RM LS + +L I + ED Y C + NP+S RS +K+ +

Sbjct: 185 QLTERMTLSQNNILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232

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FIG. 3

		Score	E
Sequences producing significant alignments:		(bits)	Value
gi 483306 pir JC1506	biliary glycoprotein B - mouse	79	1e-13
gi 111207 pir A39037	carcinoembryonic antigen mmCGM2 precu...	77	3e-13
gi 483312 pir JC1512	biliary glycoprotein H - mouse	77	4e-13
gi 13937381 ref NP_036056.1	(NM_011926) CEA-related cell a...	75	1e-12
gi 228710 prf 1809184A	pregnancy-specific glycoprotein (Ra...	70	5e-11
gi 483307 pir JC1507	biliary glycoprotein C - mouse	70	6e-11
gi 16117775 ref NP_291021.1	(NM_033543) hypothetical prote...	69	8e-11
gi 483309 pir JC1509	biliary glycoprotein E - mouse	69	9e-11
gi 312582 emb CAA47695.1	(X67278) biliary glycoprotein (Mu...	69	1e-10
gi 483311 pir JC1511	biliary glycoprotein G - mouse	68	2e-10

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FIG. 4

>gi|483306|pir||JC1506 biliary glycoprotein B - mouse

Length = 278

Score = 78.6 bits (192), Expect = 1e-13

Identities = 54/168 (32%), Positives = 86/168 (51%), Gaps = 9/168 (5%)

Query: 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 128

+ PV+ I +V GT + P + R ++ NGSLL+ + + D G Y +E +TD

Sbjct: 69 KGNPVSTNAEIVHQVTGKNKTTTGAHSGRETIVSNGSLLIQRVTVKDTGVYTIE--MTD 126

Query: 129 DTF-TGEKTINLTVDVPISRPOQLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDQKPL 187

+ F E T+ V P+++P + V +TTV EL ++ TL C N + WL + + L

Sbjct: 127 ENFRRTAATVQFHVHQPVTQPSLQVTNTTVKEL-DSVTLTCL-SNDIGANIQWLFNSQSL 184

Query: 188 LNSRMLLSPDQKVLITITRVLMEDDDLYSCVVENPISQVRSIPVKITV 235

RM LS + +L I + ED Y C + NP+S RS +K+ +

Sbjct: 185 QLTERMTLSQNNILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232

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FIG. 5

1 ATGAAGAGAG AAAGGGGAGC CCTGTCCAGA GCCTCCAGGG CCCTGCGCCT TGCTCCTTTT
m k r e r g a l s r a s r a l r l a p f

61 GTCTACCTTC TTCTGATCCA GACAGACCCC CTGGAGGGGG TGAACATCAC CAGCCCCGTG
v y l l l i q t d p l e g v n i t s p v

121 CGCTGATCC ATGGCACCGT GGGGAAGTCG GCTCTGCTTT CTGTGCAGTA CAGCAGTACC
r l i h g t v g k s a l l s v q y s s t

181 AGCAGCGACA GGCCTGTAGT GAAGTGGCAG CTGAAGCGGG ACAAGCCAGT GACCGTGGTG
s s d r p v v k w q l k r d k p v t v v

241 CAGTCCATTG GCACAGAGGT CATCGGCACC CTGCGGCCTG ACTATCGAGA CCGTATCCGA
q s i g t e v i g t l r p d y r d r i r

301 CTCTTTGAAA ATGGCTCCCT GCTTCTCAGC GACCTGCAGC TGGCCGATGA GGGCACCTAT
l f e n g s l l l s d l q l a d e g t y

361 GAGGTCGAGA TCTCCATCAC CGACGACACC TTCACTGGGG AGAAGACCAT CAACCTTACT
e v e i s i t d d t f t g e k t i n l t

421 GTAGATGTGC CCATTTCGAG GCCACAGGTG TTGGTGGCTT CAACCACTGT GCTGGAGCTC
v d v p i s r p q v l v a s t t v l e l

481 AGCGAGGCCT TCACCTTGAA CTGCTCACAT GAGAATGGCA CCAAGCCCAG CTACACCTGG
s e a f t l n c s h e n g t k p s y t w

541 CTGAAGGATG GCAAGCCCCT CCTCAATGAC TCGAGAATGC TCCTGTCCCC CGACCAAAAG
l k d g k p l l n d s r m l l s p d q k

601 GTGCTCACCA TCACCCCGGT GCTCATGGAG GATGACGACC TGTACAGCTG CATGGTGGAG
v l t i t r v l m e d d d l y s c m v e

661 AACCCCATCA GCCAGGGCCG CAGCCTGCCT GTCAAGATCA CCGTATACAG AAGAAGCTCC
n p i s q g r s l p v k i t v y r r s s

721 CTTTACATCA TCTTGTCTAC AGGAGGCATC TTCCTCCTTG TGACCTTGGT GACAGTCTGT
l y i i l s t g g i f l l v t l v t v c

781 GCCTGCTGGA AACCTCCAA AAGGAAACAG AAGAAGCTAG AAAAGCAAAA CTCCCTGGAA
a c w k p s k r k q k k l e k q n s l e

841 TACATGGATC AGAATGATGA CCGCCTGAAA CCAGAAGCAG ACACCCTCCC TCGAAGTGGT
 y m d q n d d r l k p e a d t l p r s g
 901 GAGCAGGAAC GGAAGAACCC CATG&CACTC TATATCCTGA AGGACAAGGA CTCCCCGAG
 e q e r k n p m a l y i l k d k d s p e
 961 ACCGAGGAGA ACCCGGCCCC GGAGCCTCGA AGCGCGACGG AGCCCGGCCC GCCCGGCTAC
 t e e n p a p e p r s a t e p g p p g y
 1021 TCCGTGTCTC CCGCCGTGCC CGGCCGCTCG CCGGGGCTGC CCATCCGCTC TGCCCCCGC
 s v s p a v p g r s p g l p i r s a r r
 1081 TACCCGCGCT CCCAGCGCG CTCCCCAGCC ACCGGCCGGA CACACTCGTC GCCGCCAGG
 y p r s p a r s p a t g r t h s s p p r
 1141 GCCCGAGCT CGCCCGGCCG CTCGCGCAGC GCCTCGGCA CACTGCGGAC TGCGGGCGTG
 a p s s p g r s r s a s r t l r t a g v
 1201 CACATAATCC GCGAGCAAGA CGAGGCCGGC CCGGTGGAGA TCAGCGCTG AGCCGCCTCG
 h i i r e q d e a g p v e i s a
 1261 GGATCCCCTG AGAGGCGCCC GCGGTCTGCG GCCAGTGGCC CGGGGAAAG CTGGGGCTGG
 1321 GAAGCCCGGG CGCGGCGCGC TGGGGACGAG GGGAGGTCCC GGGGGGCGC TGGTGTCTCG
 1381 GGTGTGAACG TGTATGAGCA TGCGCAGACG GAGGCGGGTG CGCGGAGGCG GCAGTGTGA
 1441 TATGGTGAAG CCGGTGCGCA TTTGCTTCG GTTTACTGGC TGTGTCTCA CTTGGTATAG
 1501 GTTGTGCCCT CTTAGGACCA CATAGATTAT TACATTCTG GCCCAATACC CAAAAGGGTT
 1561 TTATGGAAAC TAACATCAGT AACCTAACCC CCGTGAATAT CCTGTGCTCT TCCTAGGGAG
 1621 CTGTGTGTT TCCACCCAC CACCCTTCCC TCTGAACAAA TGCCTGAGTG CTGGGGCACT
 1681 TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT GCAAGTTCAG ATTAGAGAGG CCACTTTCCC
 1741 AGAATCCACA GCTGCACTAA GCTAAGGAGA AGCCAGATGC CGGTACTGG GTGTGCAGGG
 1801 GCTGTTCTGA GCTGGGGGGA TCATTGTGAA GGCCTTCTC CCTGGGACC TGGTACCTGG
 1861 GGACCTACAA GGTGGTGAGG GAAGGGTACG AGTACATTCC TTTTCCCTCT GACCTGGGCG
 1921 CTAGCAAGGG CAAAGAACCC GAGCCTGCCA GCTTGGCCTC CTCCACAGC CTCCCTCGGA
 1981 GGCATGCCAT GCCAAGCACT CTTTCTGTCT CTGTTTATGA ATAAA

FIG. 5(contd.)

FIG. 6

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gi 115886 ATGAAGAGAGAAAGGGGAGCCCTGTCCAGAGCCTCCAGGGCCCTGCGCCT 115935
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1. ATGAAGAGAGAAAGGGGAGCCCTGTCCAGAGCCTCCAGGGCCCTGCGCCT 50
 INSP052-BIP-exon1F →
 INSP052-exon2F →
 gi 115936 TGCTCCTTTTGTCTACCTTCTTCTGATCCAGACAGgtagg.....cac 115970
 ||||||||||||||||||||||||||||||||||||>>>> 10852 >>>
 51 TGCTCCTTTTGTCTACCTTCTTCTGATCCAGACAG..... 85
 ← INSP052-exon1R cont
 INSP052-exon2F cont →
 gi 115970 agACCCCTGGAGGGGGTGAACATCACCAGCCCCGTGCGCCTGATCCATG 126870
 >>||||||||||||||||||||||||||||||||||||||||||||||||||
 85. ..ACCCCTGGAGGGGGTGAACATCACCAGCCCCGTGCGCCTGATCCATG 133
 ← INSP052-exon1R
 gi 126871 GCACCGTGGGGAAGTCGGCTCTGCTTTCTGTGCAGTACAGCAGTACCAGC 126920
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 134 GCACCGTGGGGAAGTCGGCTCTGCTTTCTGTGCAGTACAGCAGTACCAGC 183
 gi 126921 AGCGACAGGCCTGTAGTGAAGTGGCAGCTGAAGCGGGACAAGCCAGTGAC 126970
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 184 AGCGACAGGCCTGTAGTGAAGTGGCAGCTGAAGCGGGACAAGCCAGTGAC 233
 gi 126971 CGTGGTGCAGTCCATTGGCACAGAGGTCATCGGCACCCTGCGGCCTGACT 127020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 234 CGTGGTGCAGTCCATTGGCACAGAGGTCATCGGCACCCTGCGGCCTGACT 283
 gi 127021 ATCGAGACCGTATCCGACTCTTTGAAAATGGCTCCCTGCTTCTCAGCGAC 127070
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 284 ATCGAGACCGTATCCGACTCTTTGAAAATGGCTCCCTGCTTCTCAGCGAC 333
 gi 127071 CTGCAGCTGGCCGATGAGGGCACCTATGAGGTCGAGATCTCCATCACC GA 127120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 334 CTGCAGCTGGCCGATGAGGGCACCTATGAGGTCGAGATCTCCATCACC GA 383

FIG. 6(contd.)

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gi 127121 CGACACCTTCACTGGGGAGAAGACCATCAACCTTACTGTAGATGgtaaa. 127164

|||||>>>>

384 CGACACCTTCACTGGGGAGAAGACCATCAACCTTACTGTAGATG..... 427

INSP052-exon3F cont

INSP052-exon2R cont

gi 127164ctcagTGCCCATTTTCGAGGCCACAGGTGTTGGTGGCTTCAACCACT 127922

717 >>>>|||||

427TGCCCATTTTCGAGGCCACAGGTGTTGGTGGCTTCAACCACT 468

INSP052-exon2R

gi 127923 GTGCTGGAGCTCAGCGAGGCCTTACCTTGAAGTGTCTCACATGAGAATGG 127972

|||||

469 GTGCTGGAGCTCAGCGAGGCCTTACCTTGAAGTGTCTCACATGAGAATGG 518

gi 127973 CACCAAGCCCAGCTACACCTGGCTGAAGGATGGCAAGCCCCCTCCTCAATG 128022

|||||

519 CACCAAGCCCAGCTACACCTGGCTGAAGGATGGCAAGCCCCCTCCTCAATG 568

gi 128023 ACTCGAGAATGCTCCTGTCCCCGACCAAAAGGTGCTCACCATCACCCGC 128072

|||||

569 ACTCGAGAATGCTCCTGTCCCCGACCAAAAGGTGCTCACCATCACCCGC 618

gi 128073 GTGCTCATGGAGGATGACGACCTGTACAGCTGCATGGTGGAGAACCCCAT 128122

|||||

619 GTGCTCATGGAGGATGACGACCTGTACAGCTGCATGGTGGAGAACCCCAT 668

gi 128123 CAGCCAGGGCCGAGCCTGCCTGTCAAGATCACCGTATACAgtgag.... 128163

|||||>>>> 295

669 CAGCCAGGGCCGAGCCTGCCTGTCAAGATCACCGTATACA..... 709

INSP052-exon3R cont

gi 128163 .cctagGAAGAAGCTCCCTTTACATCATCTTGTCTACAGGAGGCATCTTC 128502

>>>>|||||

709GAAGAAGCTCCCTTTACATCATCTTGTCTACAGGAGGCATCTTC 753

INSP052-exon3R

gi 128503 CTCCTTGTGACCTTGGTGACAGTCTGTGCCTGCTGGAAACCCTCCAAAAG 128552

|||||

754 CTCCTTGTGACCTTGGTGACAGTCTGTGCCTGCTGGAAACCCTCCAAAAG 803

FIG. 6(contd.)

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gi 128552 gtctg.....cacagGAAACAGAAGAAGCTAGAAAAGCAAACCTCCCTGG 129108
      >>>> 521 >>>>|||||
      803 .....GAAACAGAAGAAGCTAGAAAAGCAAACCTCCCTGG 838

gi 129109 AATACATGGATCAGAATGATGACCGCCTGAAACCAGAAGgtgag.....t 129147
      |||||>>>> 286 >
      839 AATACATGGATCAGAATGATGACCGCCTGAAACCAGAAG..... 877

gi 129147 gcagCAGACACCCTCCCTCGAAGTGGTGAGCAGGAACGGAAGAACCCCAT 129479
      >>>>|||||
      877 ....CAGACACCCTCCCTCGAAGTGGTGAGCAGGAACGGAAGAACCCCAT 923

gi 129480 GGCACTCTATATCCTGAAGGACAAGgtgag.....tgagGACTCCCCGG 130461
      |||||>>>> 947 >>>>|||||
      924 GGCACTCTATATCCTGAAGGACAAG.....GACTCCCCGG 958

gi 130462 AGACCGAGGAGAACCCGGCCCCGGAGCCTCGAAGCGCGACGGAGCCCGGC 130511
      |||||
      959 AGACCGAGGAGAACCCGGCCCCGGAGCCTCGAAGCGCGACGGAGCCCGGC 1008

gi 130512 CCGCCCGGGCTACTCCGTGTCTCCCGCCGTGCCCCGGCCGCTCGCCGGGGCT 130561
      |||||
      1009 CCGCCCGGGCTACTCCGTGTCTCCCGCCGTGCCCCGGCCGCTCGCCGGGGCT 1058

gi 130562 GCCCATCCGCTCTGCCCCGCCGCTACCCGCGCTCCCCAGCGCGCTCCCCAG 130611
      |||||
      1059 GCCCATCCGCTCTGCCCCGCCGCTACCCGCGCTCCCCAGCGCGCTCCCCAG 1108

gi 130612 CCACCGGCCGGACACACTCGTCGCCGCCAGGGCCCCGAGCTCGCCCGGC 130661
      |||||
      1109 CCACCGGCCGGACACACTCGTCGCCGCCAGGGCCCCGAGCTCGCCCGGC 1158

gi 130662 CGCTCGCGCAGCGCCTCGCGCACACTGCGGACTGCGGGCGTGACATAAT 130711
      |||||
      1159 CGCTCGCGCAGCGCCTCGCGCACACTGCGGACTGCGGGCGTGACATAAT 1208

gi 130712 CCGCGAGCAAGACGAGGCCGGCCCCGGTGGAGATCAGCGCCTGA 130754
      |||||
      1209 CCGCGAGCAAGACGAGGCCGGCCCCGGTGGAGATCAGCGCCTGA 1251

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FIG. 7

1 ACAAGTTTGT ACAAAAAAGC AGGCTTCGCC ACCATGAAGA GAGAAAGGGG AGCCCTGTCC
m k r e r g a l s

61 AGAGCCTCCA GGGCCCTGCG CCTTGCTCCT TTTGTCTACC TTCTTCTGAT CCAGACAGAC
r a s r a l r l a p f v y l l l i q t d

121 CCCCTGGAGG GGGTGAACAT CACCAGCCCC GTGCGCCTGA TCCATGGCAC CGTGGGGAAG
p l e g v n i t s p v r l i h g t v g k

181 TCGGCTCTGC TTTCTGTGCA GTACAGCAGT ACCAGCAGCG ACAGGCCTGT AGTGAAGTGG
s a l l s v q y s s t s s d r p v v k w

241 CAGCTGAAGC GGGACAAGCC AGTGACCGTG GTGCAGTCCA TTGGCACAGA GGTCATCGGC
q l k r d k p v t v v q s i g t e v i g

301 ACCCTGCGGC CTGACTATCG AGACCGTATC CGACTCTTTG AAAATGGCTC CCTGCTTCTC
t l r p d y r d r i r l f e n g s l l l

361 AGCGACCTGC AGCTGGCCGA TGAGGGCACC TATGAGGTCG AGATCTCCAT CACCGACGAC
s d l q l a d e g t y e v e i s i t d d

421 ACCTTCACTG GGGAGAAGAC CATCAACCTT ACTGTAGATG TGCCCATTTT GAGGCCACAG
t f t g e k t i n l t v d v p i s r p q

481 GTGTTGGTGG CTTCAACCAC TGTGCTGGAG CTCAGCGAGG CCTTCACCTT GAACTGCTCA
v l v a s t t v l e l s e a f t l n c s

541 CATGAGAATG GCACCAAGCC CAGCTACACC TGGCTGAAGG ATGGCAAGCC CCTCCTCAAT
h e n g t k p s y t w l k d g k p l l n

601 GACTCGAGAA TGCTCCTGTC CCCCACCAA AAGGTGCTCA CCATCACCCG CGTGCTCATG
d s r m l l s p d q k v l t i t r v l m

661 GAGGATGACG ACCTGTACAG CTGCATGGTG GAGAACCCCA TCAGCCAGGG CCGCAGCCTG
e d d d l y s c m v e n p i s q g r s l

721 CCTGTCAAGA TCACCGTATA CAGAAGAAGC TCCCACCATC ACCATCACCA TTGAAACCCA
p v k i t v y r r s s h h h h h h -

781 GCTTTCTTGT ACAAAGTGGT

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FIG. 8

Molecule: pENTR-INSP052- EC-6HIS, 3005 bps DNA Circular
File Name: pENTR-INSP052-6HIS.cm5, dated 21 Feb 2003

Description: Ligation of Cons-6His.SEQ into pENTR-attL1-attL2

Molecule Features:

Type	Start	End	Name	Description
MARKER	21			pENTR-F1 primer
MARKER	110		C attL1	
GENE	136	873	INSP052-EC-6HIS	
MARKER	888		attL2	
MARKER	1001		C	pENTR-R1 primer
GENE	1100	1909	KanR	
REGION	2030	2669	ori	

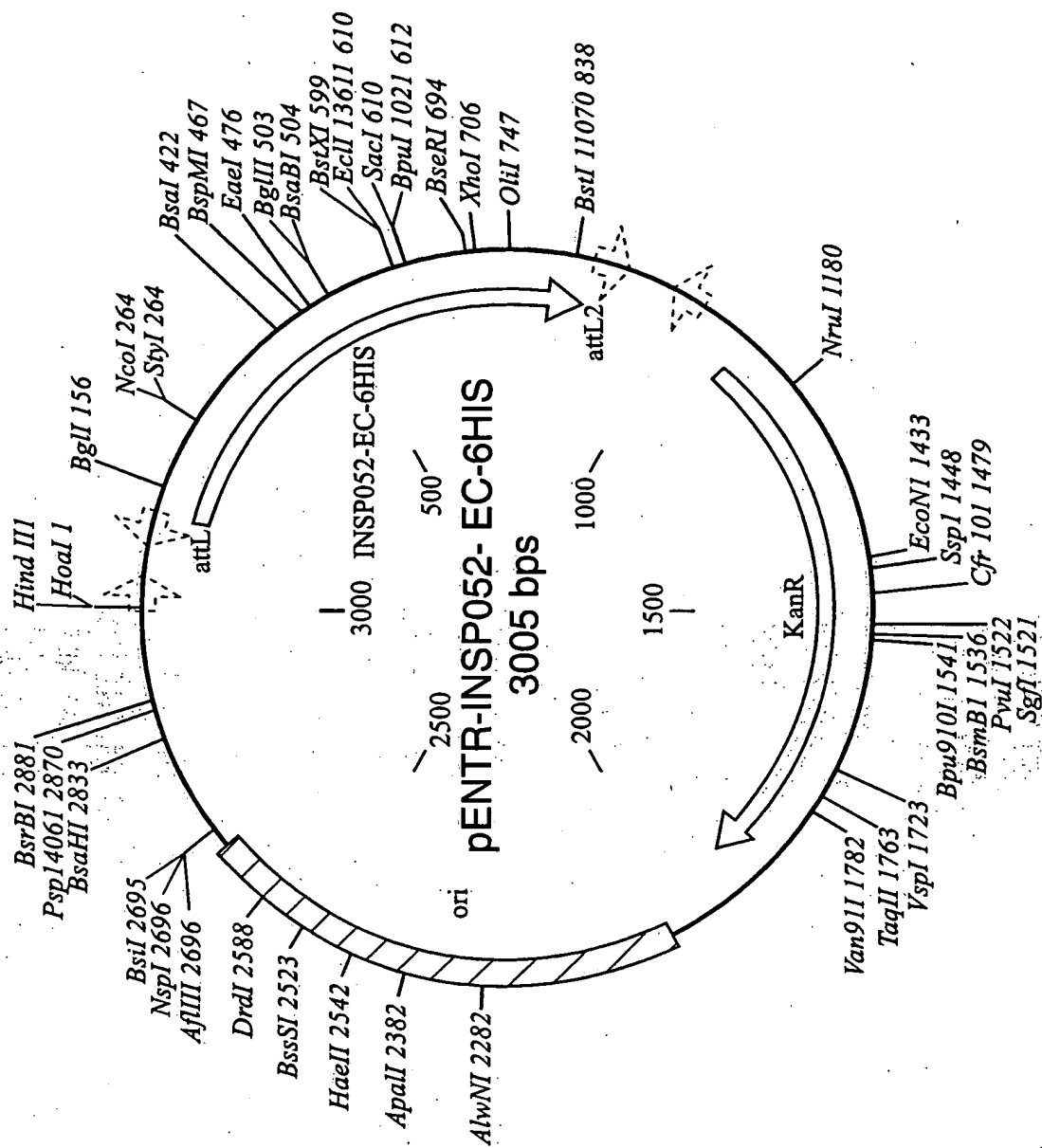


FIG. 8(contd.)

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FIG. 9

Molecule: pEAK12d-INSP052-EC-6HIS, 7687 bps DNA Circular

File Name: pEAK12d-INSP052-6HIS.cm5, dated 21 Feb 2003

Description: Ligation of Cons-6His.SEQ into pEAK12d-attB1-attB2

Molecule Features:

Type	Start	End	Name	Description
REGION	2	595		pmb-ori
GENE	596	1519	AmpR	
REGION	1690	2795	EF-1a	
MARKER	2703			pEAK12F primer
REGION	2855	2887	attB1	
GENE	2888	3625	INSP052-EC-6HIS (aal-240)	
REGION	3629	3654	attB2	
MARKER	3656		C	pEAK12R primer
REGION	3661	4089		poly A/splice
GENE	4708	4090	C	PUROMYCIN resistance
REGION	4932	4709	C tk	tk promoter
REGION	5427	4933	C Ori P	
GENE	7479	5427	C EBNA-1	
REGION	7480	7679	sv40	

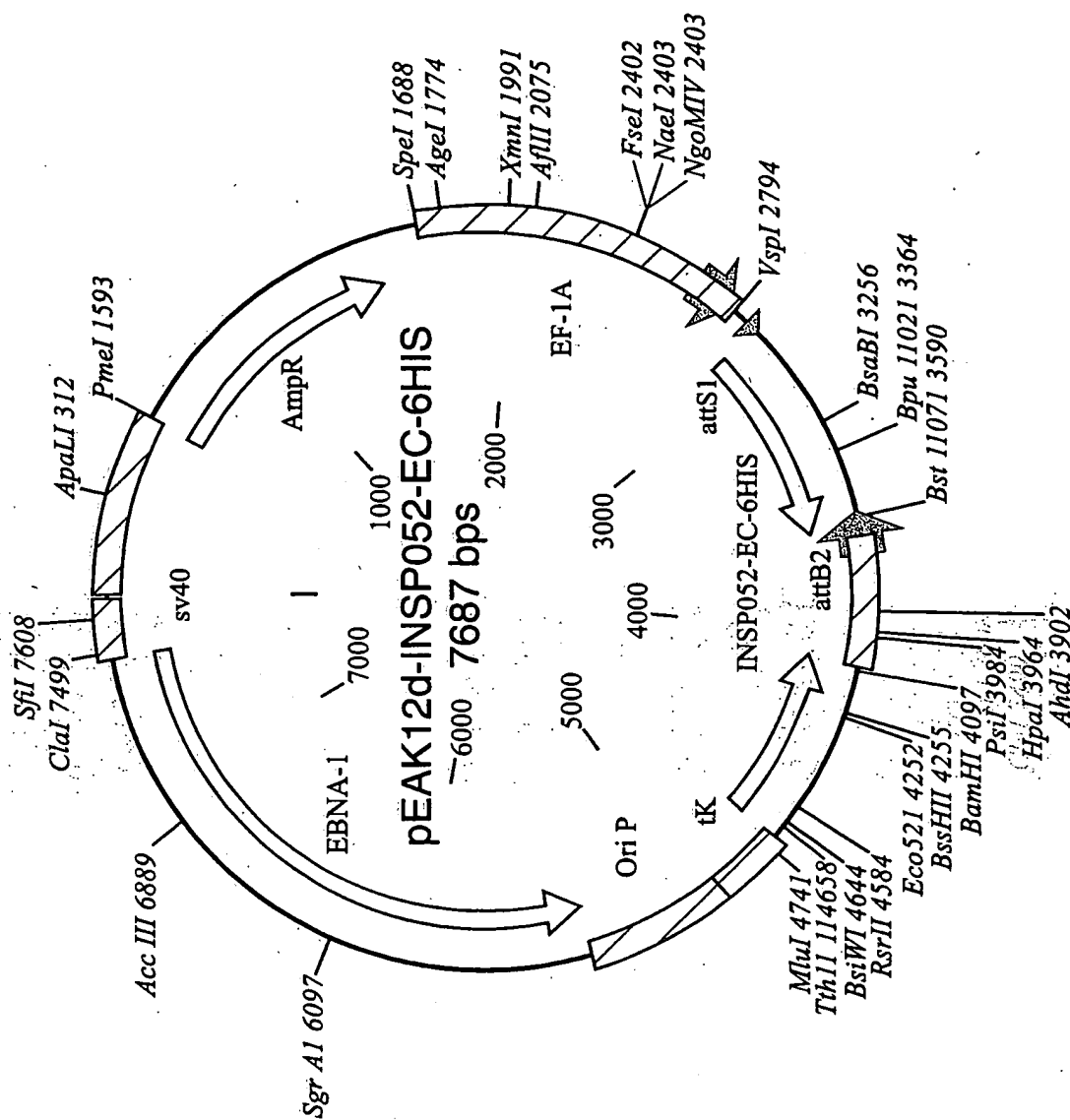
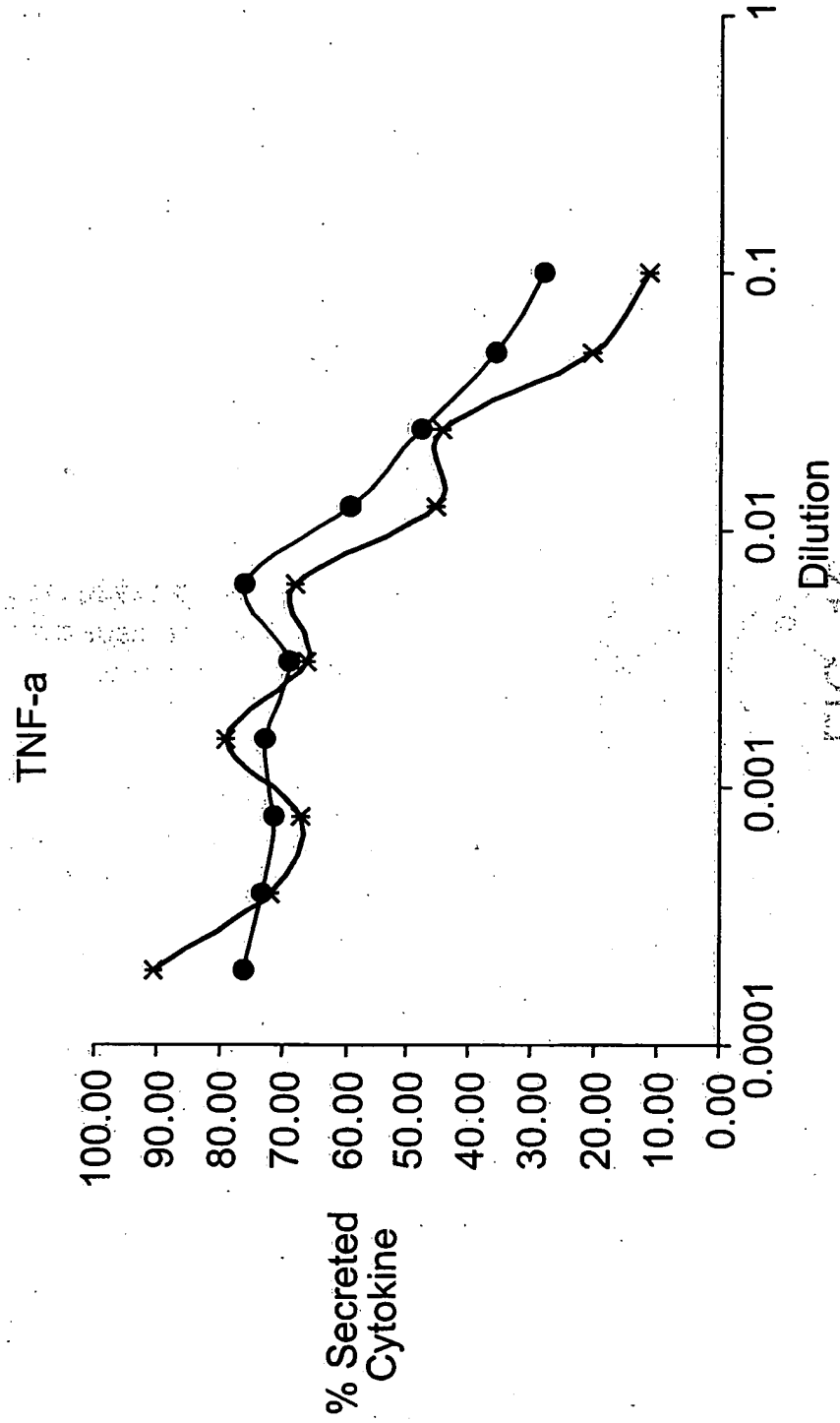


FIG. 9(contd.)

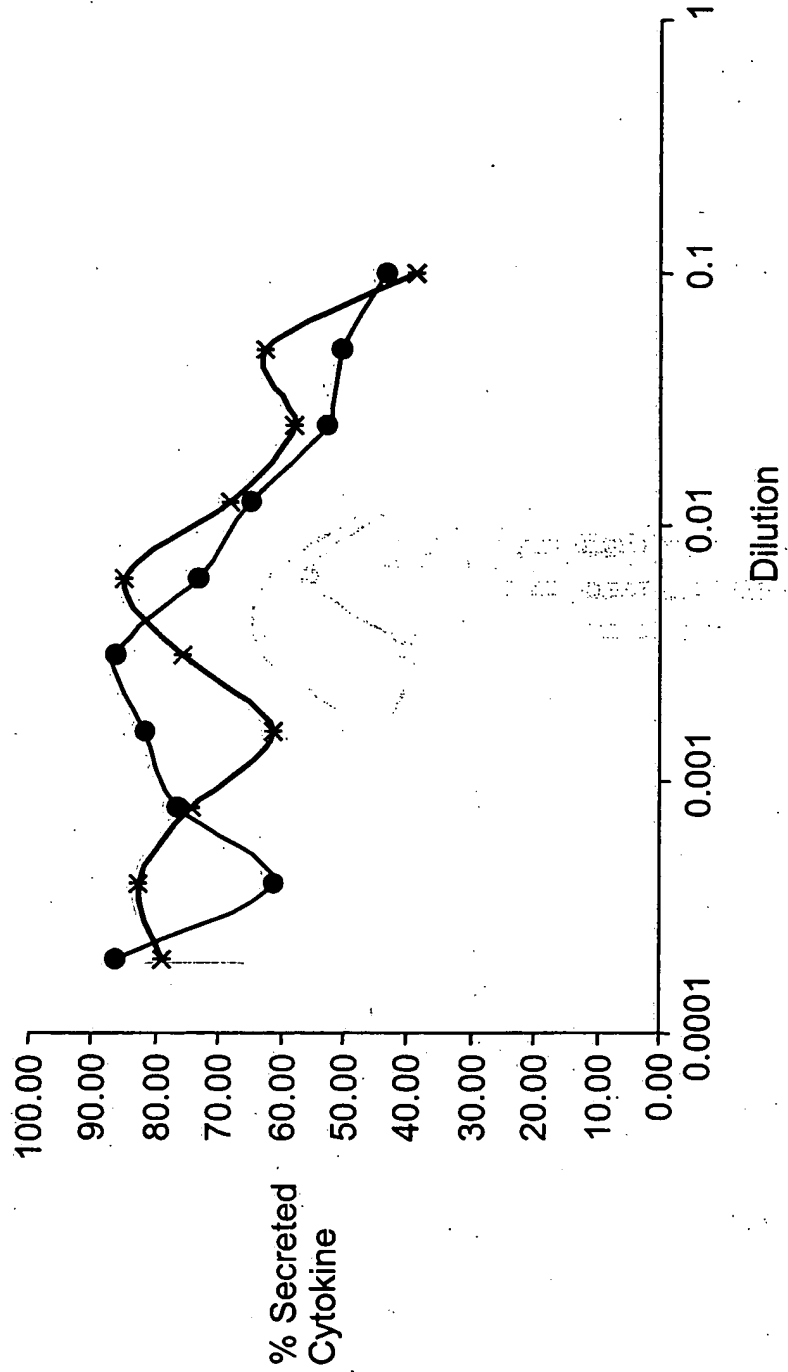
FIG. 10



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FIG. 11

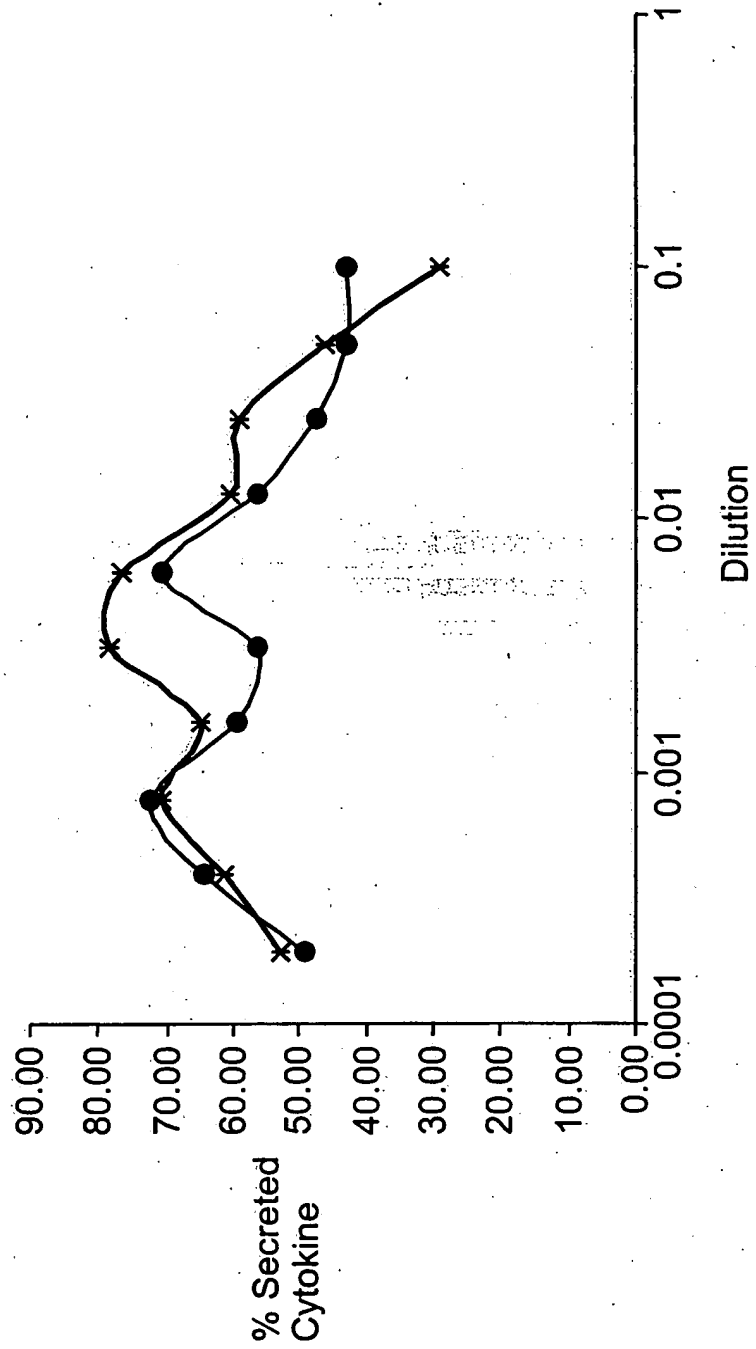
IL-4



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FIG. 12

IL-2



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FIG. 13A

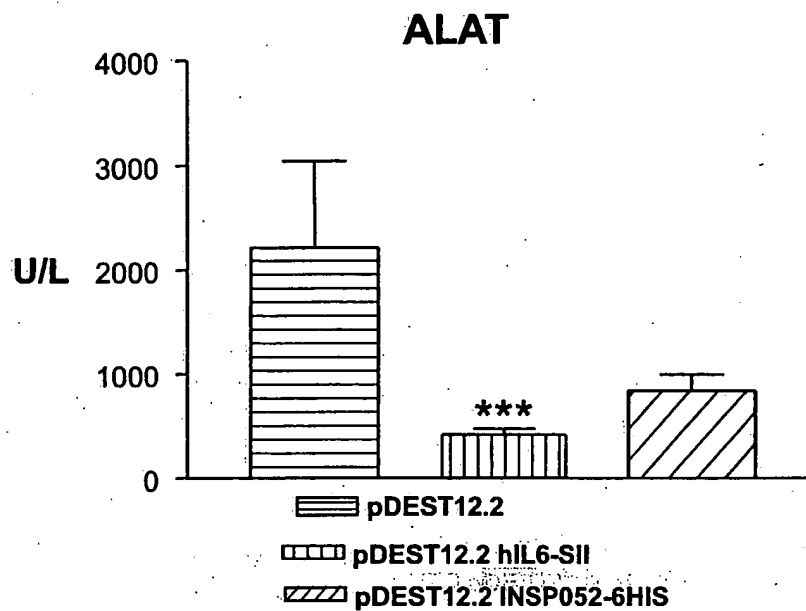
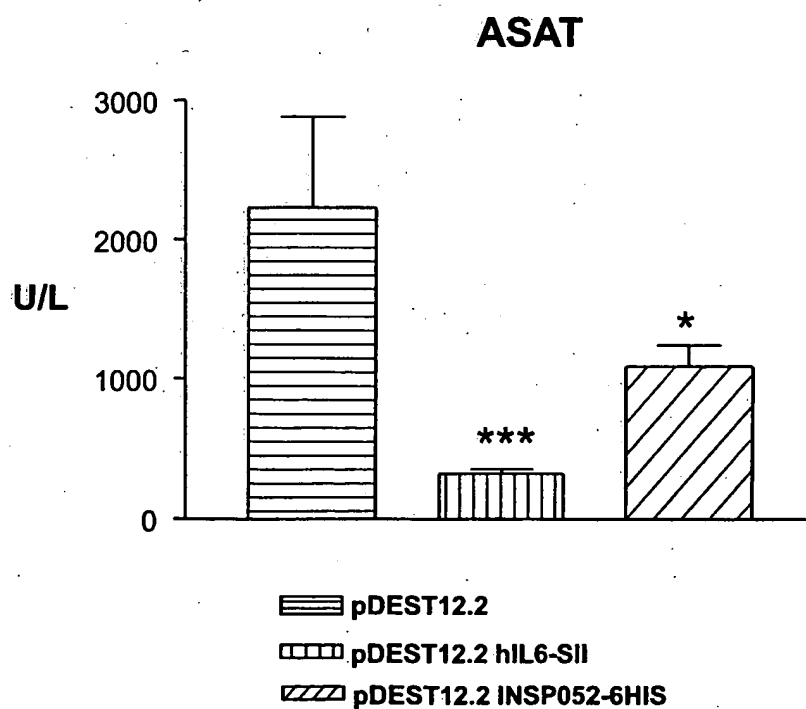


FIG. 13B



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FIG. 14A

TNF 1h30

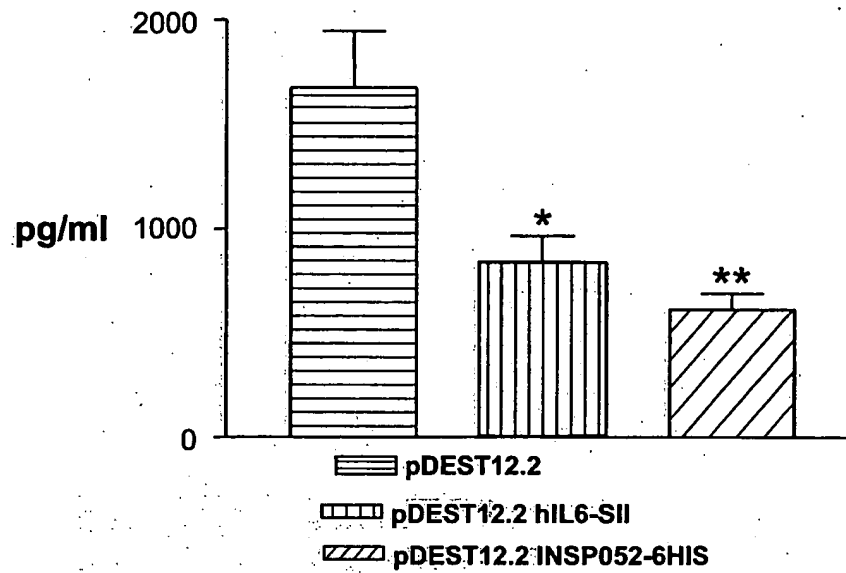
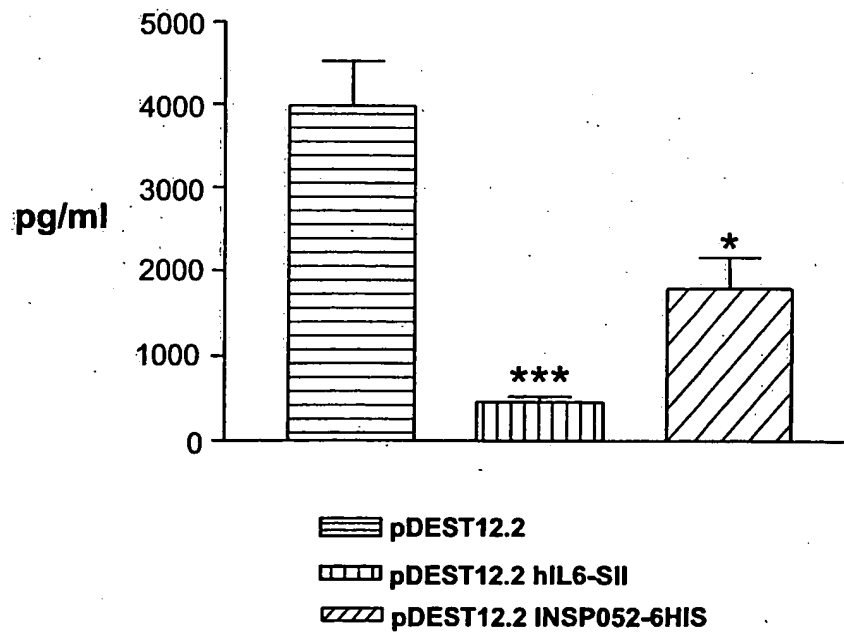


FIG. 14B

mIL6 8h



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FIG. 15A

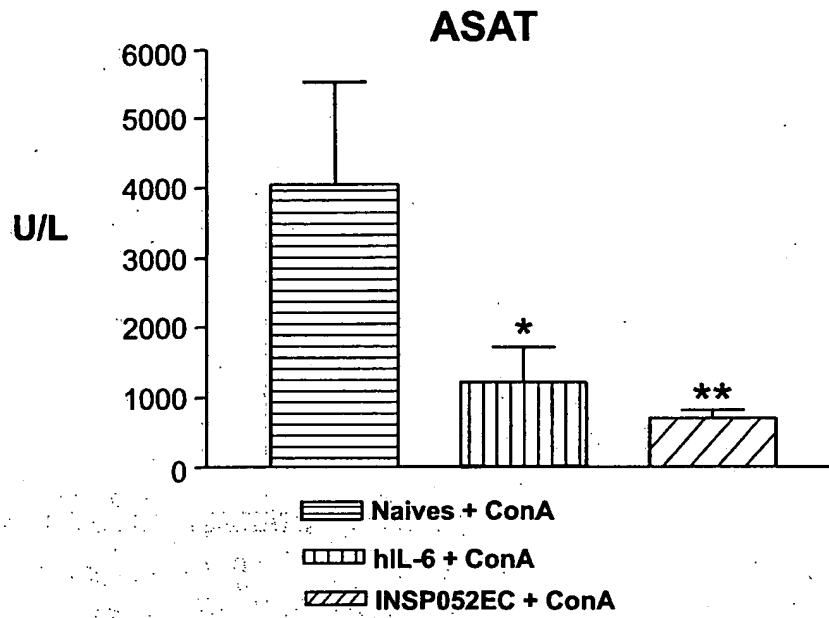
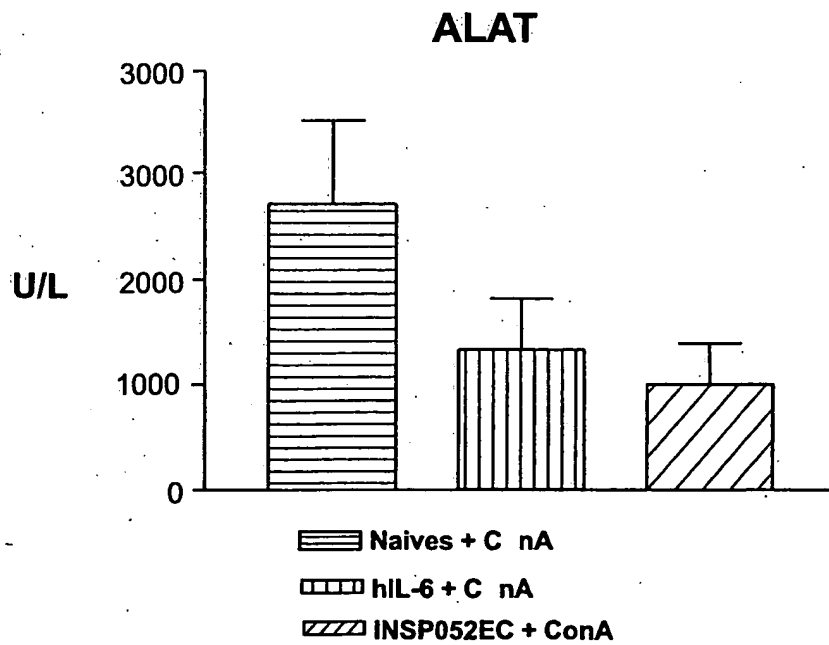


FIG. 15B



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FIG. 15C

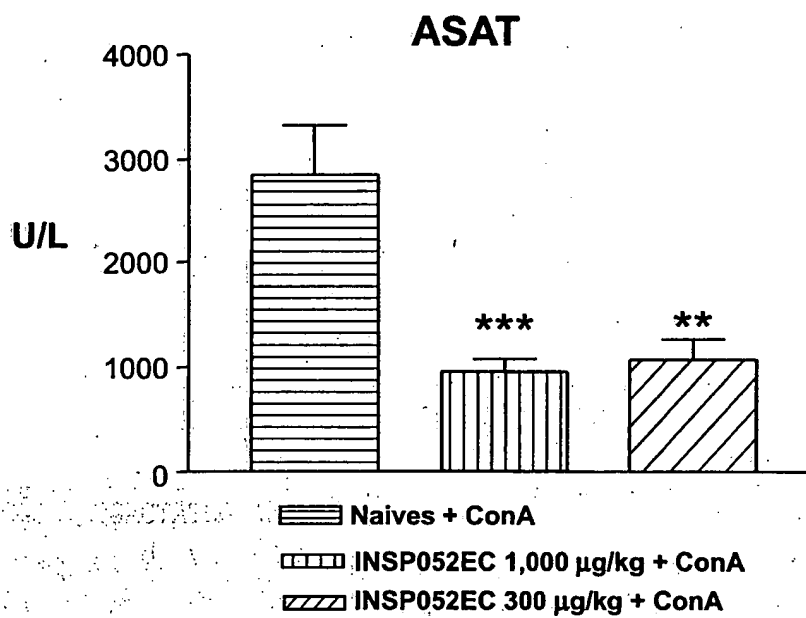


FIG. 15D

